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(54) Title: MOLECULES EXPRESSED IN HIPPOCAMPUS

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      10      19      28      37      46      55
5' CCAG GCA CCT GAC GCC TCT TTC CCC TCA CGG TGC CAG GGC CGG GCC GAA CTA CAT

      64      73      82      91      100      109
TTC CCA GGA GGC TCC GCG GCC AGG TGC AAA CAG CGC CGT GCT GAC TAC ATT TCC

      118      127      136      145      154      163
CAG ACA GCC TTG CGG CGG CCC GGG CCT TAA AGC GTC CAT TTC CCA GCG GCC CTC

      172      181      190      199      208      217
CGC TGC GAG ACC GCA GCC CTT CTC TGG AGT CTC AGA GCC GCA AGA CAC CAC GAC

      226      235      244      253      262      271
TCC CAG AGG ACC TTG CGT CGG GCA AGA AAG ACT ACA CCT TCC AGA GGC CTC TGC

      280      289      298      307      316      325
GGC GCC GCG ACA GGA AGC GGC GGG CGA GCC GAG TGT CCT TGC GCG TGG ATC CGA
  
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(57) Abstract

The invention provides novel developmentally-regulated hippocampal genes and polypeptides encoded by those genes. The invention also provides expression vectors, host cells, and antibodies. The invention also provides methods for diagnosing, treating or preventing diseases associated with hippocampus.

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MOLECULES EXPRESSED IN HIPPOCAMPUS

TECHNICAL FIELD

The present invention relates to polynucleotides comprising at least a fragment of genes
5 expressed in hippocampus. The invention also relates to the use of these molecules in diagnosis,
prognosis, prevention, treatment, and evaluation of therapies for diseases associated with the
hippocampus such as Alzheimer's disease, Huntington's disease, schizophrenia, and epilepsy.

BACKGROUND ART

The hippocampus is part of the brain's limbic system which controls emotional behavior,
10 motivational drive, and other physiological functions. The limbic system includes the limbic cortex,
hippocampus, amygdala, hypothalamus, and anterior thalamus. The hippocampus plays an
important role in learning processes and certain types of memory. Stimulation of the hippocampus
can cause behavioral responses including rage, passivity, and excess sex drive. Weak electrical
stimulation can cause hippocampal seizures. Individuals who lose hippocampal function retain
15 memory for events that occurred prior to the loss and only have immediate memory, lasting less than
a few minutes, for all events after the loss (anterograde amnesia). Thus, the hippocampus is thought
to interpret the importance of incoming sensory information and to determine what input is worth
remembering. The hippocampus then transmits signals that make the mind rehearse the information
over and over again until permanent storage takes place.

20 Numerous studies of the effects of ablation of the hippocampus of rodent, primate, and
other non-human species have been conducted. Memory disorders and spatial performance are
associated with hippocampal function. Morphological changes in the hippocampus, including cell
loss, is associated with epilepsy, schizophrenia, Alzheimer's disease, and certain amnesiac
syndromes (Jack (1994) *Epilepsia* 35:S21-S29). Research data from animals show glucocorticoids
25 secreted during stress can damage the hippocampus and impair the ability of hippocampal neurons
to survive neurological insults (Sapolsky (1993) *Behav. Brain Res.* 57:175-82). Sustained
glucocorticoid exposure might damage the hippocampus in humans as well; hippocampal atrophy
has been reported in patients with Cushing's syndrome as a result of the hypersecretion of
glucocorticoids.

30 Phylogenetic relationships among organisms have been demonstrated many times, and
studies from a diversity of prokaryotic and eukaryotic organisms suggest a more or less gradual
evolution of biochemical and physiological mechanisms and metabolic pathways. Despite different
evolutionary pressures, proteins that regulate the cell cycle in yeast, nematode, fly, rat, and man
have common chemical or structural features and modulate the same general cellular activity.

35 Comparisons of human gene sequences with those from other organisms where the structure and/or

function may be known allow researchers to draw analogies and to develop model systems for testing hypotheses. These model systems are of great importance in developing and testing diagnostic and therapeutic agents for human conditions, diseases and disorders.

Identification of genes that participate in hippocampal development provide new potential
5 diagnostic and therapeutic targets. The present invention satisfies a need in the art by providing new compositions that are useful for diagnosis, prognosis, treatment, prevention, and evaluation of therapies for diseases associated with hippocampus such as Alzheimer's disease, Huntington's disease, schizophrenia, epilepsy.

SUMMARY OF THE INVENTION

10 In one aspect, the invention provides for substantially purified polynucleotides expressed in hippocampus. Preferred embodiments include (a) a polynucleotide sequence of SEQ ID NOs:1-7; (b) a polynucleotide sequence which encodes the polypeptide sequence of SEQ ID NO:8; (c) a polynucleotide sequence having at least 70% identity to the polynucleotide sequence of (a) or (b); (d) a polynucleotide sequence which is complementary to the polynucleotide sequence of (a), (b), or (c);
15 (e) a polynucleotide sequence comprising at least 10, preferably at least 18, sequential nucleotides of the polynucleotide sequence of (a), (b), (c), or (d); and (f) a polynucleotide which hybridizes under stringent conditions to the polynucleotide of (a), (b), (c), (d) or (e). Furthermore, the invention provides an expression vector comprising any of the above described polynucleotides and host cells comprising the expression vector. Still further, the invention provides a method for
20 treating or preventing a disease or condition associated with the altered expression of a gene that is expressed in hippocampus comprising administering to a subject in need a polynucleotide described above in an amount effective for treating or preventing the disease.

In a second aspect, the invention provides a substantially purified polypeptide comprising the gene product of a gene that is expressed in hippocampus. Preferred embodiments are (a) the
25 polypeptide sequence of SEQ ID NO:8; (b) a polypeptide sequence having at least 85% identity to the polypeptide sequence of (a); and (c) a polypeptide sequence comprising at least 6 sequential amino acids of the polypeptide sequence of (a) or (b). Additionally, the invention provides antibodies that bind specifically to the above described polypeptide and a method for treating or preventing a disease or condition associated with the altered expression of a gene that is expressed in
30 hippocampus comprising administering to a subject in need such an antibody in an amount effective for treating or preventing the disease.

In another aspect, the invention provides a pharmaceutical composition comprising any one of the polynucleotides or polypeptides described above in conjunction with a suitable pharmaceutical carrier and a method for treating or preventing a disease or condition associated
35 with the altered expression of a gene that is expressed in hippocampus comprising administering to a

subject in need such a composition in an amount effective for treating or preventing the disease.

In a further aspect, the invention provides a method for diagnosing a disease or condition associated with the altered expression of a gene that is expressed in hippocampus. The method comprises the steps of (a) providing a sample comprising one or more of the expressed genes; (b) hybridizing one or more of the polynucleotides described above to the expressed genes under conditions effective to form one or more hybridization complexes; (c) detecting the hybridization complexes; and (d) comparing the levels of the hybridization complexes with the level of hybridization complexes in a nondiseased sample, wherein altered levels of one or more of the hybridization complexes in a diseased sample compared with the level of hybridization complexes in a non-diseased sample correlates with the presence of the disease or condition.

The invention also provides a method for using a nucleic acid or a fragment thereof to screen a library of molecules to identify at least one molecule which specifically binds the nucleic acid, the method comprising providing a library of molecules, combining the nucleic acid with the library of molecules under conditions suitable to allow specific binding, and detecting specific binding, thereby identifying a molecule which specifically binds the nucleic acid. Such libraries include DNA and RNA molecules, peptides, peptide nucleic acids, proteins, and the like which are potential regulators of replication, transcription, and translation. The invention also provides a method for using a protein or a portion thereof to screen a library of molecules to identify at least one molecule which specifically binds the protein, the method comprising providing a library of molecules, combining the protein with the library of molecules under conditions suitable to allow specific binding, and detecting specific binding, thereby identifying a molecule which specifically binds the protein. In one aspect, a molecule identified using the method modulates the activity of the protein.

Additionally, the invention provides antibodies, antibody fragments, and immunoconjugates that exhibit specificity to the above described polypeptide and methods for treating or preventing a disease or condition associated with hippocampus.

BRIEF DESCRIPTION OF THE SEQUENCE LISTING

The Sequence Listing provides exemplary sequences of genes expressed in adult rat hippocampus, SEQ ID NOs:9-15, and homologous human sequences including polynucleotide sequences, SEQ ID NOs:1-7, and polypeptide sequence, SEQ ID NO:8. Each sequence is identified by a sequence identification number (SEQ ID NO) and by the Incyte Clone number with which the sequence was first identified.

Table 1 shows the Incyte clone number for nucleic acid sequences expressed in adult rat hippocampus but absent from fetal rat hippocampus; the Incyte clone number and SEQ ID NO: for the human nucleic acid homolog; the location of a unique region of the human nucleic acid sequence:

the sequence identity between the rat sequence and corresponding human sequence; and the tissues where the human sequence is predominantly expressed.

Figures 1A, 1B, and 1C show the nucleic acid sequence of SEQ ID NO:7 and encoded amino acid sequence, SEQ ID NO:8. The alignment was produced using MACDNASIS PRO
5 software (Hitachi Software Engineering, South San Francisco CA).

DESCRIPTION OF THE INVENTION

It must be noted that as used herein and in the appended claims, the singular forms "a", "an", and "the" include the plural reference unless the context clearly dictates otherwise. Thus, for example, a reference to "a host cell" includes a plurality of such host cells, and a reference to "an
10 antibody" is a reference to one or more antibodies and equivalents thereof known to those skilled in the art, and so forth.

DEFINITIONS

"NSEQ" refers generally to a polynucleotide sequence of the present invention, including SEQ ID NOs:1-7. "PSEQ" refers generally to a polypeptide sequence of the present invention.
15 including SEQ ID NO:8.

A "fragment" can refer to a nucleic acid sequence that is preferably at least 20 nucleic acids in length, more preferably 40 nucleic acids, and most preferably 60 nucleic acids in length, and encompasses, for example, fragments consisting of nucleic acids 1-50, 51-400, 401-4000, 4001-12,000, and the like, of SEQ ID NOs:1-7.

20 "Gene" or "gene sequence" refers to the partial or complete coding sequence of a gene, its complement, and its 5' or 3' untranslated regions.

"Homology" refers to sequence similarity between a reference sequence and at least a fragment of a newly sequenced clone insert or its encoded amino acid sequence.

"Polynucleotide" refers to a nucleic acid, nucleic acid sequence, oligonucleotide, nucleotide,
25 or any fragment thereof. It may be DNA or RNA of genomic or synthetic origin, double-stranded or single-stranded, and combined with carbohydrate, lipids, protein or other materials to perform a particular activity or form a useful composition. "Oligonucleotide" is substantially equivalent to the terms amplicon, primer, oligomer, element, and probe.

"Polypeptide" refers to an amino acid, amino acid sequence, oligopeptide, peptide, or
30 protein or portions thereof whether naturally occurring or synthetic.

A "portion" refers to an amino acid sequence which is preferably at least 5 to about 15 amino acids in length, most preferably at least 10 amino acids long, and which retains some biological or immunological activity of, for example, SEQ ID NO:8.

"Sample" is used in its broadest sense. A sample containing nucleic acids may comprise a
35 bodily fluid; an extract from a cell, chromosome, organelle, or membrane isolated from a cell;

genomic DNA, RNA, or cDNA in solution or bound to a substrate; a cell; a tissue; a tissue print; and the like.

“Substantially purified” refers to a nucleic acid or an amino acid sequence that is removed from its natural environment and that is isolated or separated, and is at least about 60% free, preferably about 75% free, and most preferably about 90% free, from other components with which it is naturally present.

“Substrate” refers to any suitable rigid or semi-rigid support to which polynucleotides or polypeptides are bound and includes membranes, filters, chips, slides, wafers, fibers, magnetic or nonmagnetic beads, gels, capillaries or other tubing, plates, polymers, and microparticles with a variety of surface forms including wells, trenches, pins, channels and pores.

A “variant” refers to a polynucleotide or polypeptide whose sequence diverges from SEQ ID NOs:1-7 or SEQ ID NO:8, respectively. Polynucleotide sequence divergence may result from mutational changes such as deletions, additions, and substitutions of one or more nucleotides; it may also be introduced to accommodate differences in codon usage. Each of these types of changes may occur alone, or in combination, one or more times in a given sequence. Polypeptide variants include sequences that possess at least one structural or functional characteristic of SEQ ID NO:8.

DETAILED DESCRIPTION

Sequences in the present invention were first identified by comparing polynucleotides expressed in a fetal rat hippocampus-derived cDNA library to polynucleotides expressed in an adult rat hippocampus-derived cDNA library. Since some of the polynucleotide sequences were identified solely based on expression levels, it is not essential to know a priori the function of a particular gene in hippocampus. The abundance sort program of the invention described in USPN 5,840,484, entitled “Comparative Gene Transcript Analysis”, incorporated herein by reference, was used to tabulate and sort by frequency the mRNA transcripts corresponding to each gene identified in rat fetal and adult hippocampal tissues. Comparative gene transcript analysis was also employed to identify genes differentially expressed in adult rat hippocampus but not in fetal rat hippocampus.

After assembling EST clusters, a transcript image for each cDNA library was generated and the frequency or abundance of a given EST cluster was determined. The frequency of an EST cluster in a clone population correlated to the level of expression of a particular gene. Transcript analysis summarized the presence and abundance of exact, unique, and homologous transcripts which were specific to each tissue sample. Polynucleotides expressed only in adult rat hippocampus were used to identify homologous sequences from human. The human nucleic acid sequences, SEQ ID NOs:1-7, the amino acid sequence corresponding to SEQ ID NO:7, SEQ ID NO:8, and the rat nucleic acid sequences, SEQ ID NOs:9-15, are provided in the Sequence Listing.

Table 1 shows the nucleic acid sequences expressed in adult rat hippocampus but absent

from fetal rat hippocampus. SEQ ID NOs:9-15, and their human homologs. SEQ ID NOs:1-7.

Column 1 lists the Incyte clone number for each nucleic acid sequence, SEQ ID NOs:9-15, expressed in adult rat hippocampus but absent from fetal rat hippocampus first identified. These nucleic acid sequences were used to identify the human nucleic acid sequences shown in column 3.

5 Columns 2 and 3 list the SEQ ID NO: and corresponding Incyte clone number, respectively, for each human nucleic acid sequence. Fragments of SEQ ID NOs:1-7 are useful in hybridization or amplification technologies to identify changes in expression pattern of the same or similar sequences. Column 4 shows exemplary fragments for SEQ ID NOs:1-7. Column 5 shows the sequence identity between the rat nucleic acid sequence in column 4 and the corresponding human
10 nucleic acid sequence in column 2. Column 6 identifies the human tissues where the sequences in column 3 are predominantly expressed. All of the human sequences are expressed in nervous tissue, including hippocampus.

Therefore, in one embodiment, the invention encompasses a polynucleotide sequence (NSEQ) comprising the sequence of SEQ ID NOs:1-7. These 7 polynucleotides are shown by the
15 method of the present invention to have strong differential expression association with adult hippocampus. The invention also encompasses a variant of the polynucleotide sequence, its complement, or 18 consecutive nucleotides of a sequence provided in the above described sequences. Variant polynucleotide sequences typically have at least about 70%, more preferably at least about 85%, and most preferably at least about 95% polynucleotide sequence identity to NSEQ.

20 The invention provides polynucleotide sequences comprising at least a fragment of one or more genes expressed in hippocampus. The polynucleotide sequences are useful for screening libraries of molecules for specific binding and for diagnosis and prognosis of diseases of the hippocampus, such as Alzheimer's disease, Huntington's disease, schizophrenia, epilepsy, and their complications.

25 The polynucleotide sequences are particularly useful when they are hybridizable array elements in a microarray. Such a microarray can be employed to monitor the expression of genes which are differentially expressed in fetal, normal, diseased, or treated hippocampus. The microarray can be used in large scale genetic or gene expression analysis of a large number of polynucleotide sequences; in the diagnosis of diseases before phenotypic symptoms are evident; or in
30 the differential diagnosis of diseases with similar symptoms. The microarray can also be used in the monitoring and evaluation of treatments where altered expression of genes coding for polypeptides implicated in hippocampus function cause disease, such as epilepsy. Additionally, the microarray can be used to investigate an individual's predisposition to a disease, such as Alzheimer's disease. Furthermore, the microarray can be employed to investigate cellular responses, such as nerve cell
35 proliferation, regeneration, degeneration, and the like.

When the polynucleotide sequences of the invention are employed as hybridizable array elements in a microarray, the array elements are organized in an ordered fashion so that each element is present at a specified location on the substrate. Because the array elements are at specified locations on the substrate, the hybridization patterns and intensities (which together create a unique expression profile) can be interpreted in terms of expression levels of particular genes and can be correlated with a particular disease, condition, or treatment.

The invention also entails a pharmaceutical composition comprising a polynucleotide sequence of the invention in conjunction with a suitable pharmaceutical carrier and a method for treating or preventing a disease or condition associated with the altered expression of genes that regulate the hippocampus comprising administering to a subject in need such a composition in an amount effective for treating or preventing a disease or condition associated with hippocampus.

After assembling EST clusters, a transcript image for each cDNA library is generated, and the frequency or abundance of a given EST cluster is determined. The frequency of an EST cluster in a clone population is correlated to the level of expression of a particular gene. Transcript analysis summarizes the presence and abundance of exact, unique, and homologous transcripts which are specific to each tissue sample. Comparison of transcript images derived from different biological samples can demonstrate a statistically significant correlation between cell and tissue source information, such as disease states, treatment outcomes, exposure to various environmental factors, genotypes, and the expression levels of particular genes or groups of genes. Comparisons between transcript images of different cells or tissues or of the same cells or tissues under different conditions can be used to discern differences in transcriptional activities. For example, a transcript image may show the following differences: a) differences between hippocampus and frontal cortex; b) differences between normal and diseased brain tissue, or c) differences between untreated and treated brain tissue.

Transcript image comparisons can be obtained by methods well known to those skilled in the art. Transcript levels and images can be obtained and compared, for example, by a differential gene expression assay based on a quantitative hybridization of arrayed DNA clones (Nguyen *et al.* (1995) Genomics 29:207-216), based on the serial analysis of gene expression (SAGE) technology (Velculescu *et al.* (1995) Science 270:484-487), based on the polymerase chain reaction (Peng *et al.* (1992) Science 257:967-971; Prashar *et al.* (1996) Proc. Natl. Acad. Sci. 93:659-663), based on a differential amplification protocol (Van Gelder *et al.* USPN 5,545,522), or based on electronic analysis, such as comparative gene transcript analysis (Seilhamer *et al.* USPN 5,840,484) or the GEMTOOLS gene expression analysis program (Incyte Pharmaceuticals, Palo Alto CA). Preferably, comparisons between two or more transcript profiles are performed electronically.

Specifically, transcript profiles can be compared to identify polynucleotide sequences whose

transcripts (1) are present only in fetal hippocampus, (2) are present only in adult hippocampus, (3) are expressed at higher levels in fetal hippocampus than in adult hippocampus, (4) are expressed at higher levels in adult hippocampus than in fetal hippocampus, (5) are present in other rat tissue, such as liver, but not present in fetal hippocampus nor adult hippocampus, and (6) are present in both fetal hippocampus and adult hippocampus and show no statistically significant differences in expression when comparing tissues.

NSEQ or the encoded PSEQ may be used to search against the GenBank primate (pri), rodent (rod), mammalian (mam), vertebrate (vrtp), and eukaryote (eukp) databases, SwissProt, BLOCKS (Bairoch *et al.* (1997) *Nucleic Acids Res.* 25:217-221), PFAM, and other databases that contain previously identified and annotated motifs, sequences, and gene functions. Methods that search for primary sequence patterns with secondary structure gap penalties (Smith *et al.* (1992) *Protein Engineering* 5:35-51) as well as algorithms such as Basic Local Alignment Search Tool (BLAST; Altschul (1993) *J. Mol. Evol.* 36:290-300; Altschul *et al.* (1990) *J. Mol. Biol.* 215:403-410), BLOCKS (Henikoff and Henikoff (1991) *Nucleic Acids Res.* 19:6565-6572), Hidden Markov Models (HMM; Eddy (1996) *Cur. Opin. Str. Biol.* 6:361-365; Sonnhammer *et al.* (1997) *Proteins* 28:405-420), and the like, can be used to manipulate and analyze nucleotide and amino acid sequences. These databases, algorithms and other methods are well known in the art and are described in Ausubel *et al.* (1997; *Short Protocols in Molecular Biology*, John Wiley & Sons, New York NY, unit 7.7) and in Meyers (1995; *Molecular Biology and Biotechnology*, Wiley VCH, New York NY, p 856-853).

Also encompassed by the invention are polynucleotide sequences that are capable of hybridizing to SEQ ID NOs:1-7, and fragments thereof under stringent conditions. Stringent conditions can be defined by salt concentration, temperature, and other chemicals and conditions well known in the art. Suitable conditions can be selected, for example, by varying the concentrations of salt in the prehybridization, hybridization, and wash solutions or by varying the hybridization and wash temperatures. With some substrates, the temperature can be decreased by adding formamide to the prehybridization and hybridization solutions.

Hybridization can be performed at low stringency with buffers, such as 5xSSC with 1% sodium dodecyl sulfate (SDS) at 60° C, which permits complexes to form between two nucleic acid sequences that contain some mismatches. Subsequent washes are performed at higher stringency with buffers such as 0.2xSSC with 0.1% SDS at either 45° C (medium stringency) or 68° C (high stringency), to maintain hybridization of only those complexes that contain completely complementary sequences. Background signals can be reduced by the use of detergents such as SDS, Sarcosyl, or Triton X-100, and/or a blocking agent, such as salmon sperm DNA. Hybridization methods are described in detail in Ausubel (*supra*, units 2.8-2.11, 3.18-3.19 and 4-6-

4.9) and Sambrook et al. (1989; Molecular Cloning. A Laboratory Manual, Cold Spring Harbor Press, Plainview NY)

NSEQ can be extended utilizing a partial nucleotide sequence and employing various PCR-based methods known in the art to detect upstream sequences such as promoters and other regulatory elements. (See, e.g., Dieffenbach and Dveksler (1995) PCR Primer, a Laboratory Manual, Cold Spring Harbor Press, Plainview NY). Additionally, one may use an XL-PCR kit (PE Biosystems, FosterCity CA), nested primers, and commercially available cDNA (Life Technologies, Rockville MD) or genomic libraries (Clontech, Palo Alto CA) to extend the sequence. For all PCR-based methods, primers may be designed using commercially available software, such as OLIGO 4.06 software (National Biosciences, Plymouth MN) or another appropriate program, to be about 18 to 30 nucleotides in length, to have a GC content of about 50%, and to form a hybridization complex at temperatures of about 68°C to 72°C.

In another aspect of the invention, NSEQ can be cloned in recombinant DNA molecules that direct the expression of PSEQ or structural or functional fragments thereof, in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences which encode substantially the same or a functionally equivalent amino acid sequence may be produced and used to express the polypeptide encoded by NSEQ. The nucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter the nucleotide sequences for a variety of purposes including, but not limited to, modification of the cloning, processing, and/or expression of the gene product. DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide sequences. For example, oligonucleotide-mediated site-directed mutagenesis may be used to introduce mutations that create new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, and so forth.

In order to express a biologically active protein, NSEQ, or derivatives thereof, may be inserted into an appropriate expression vector, i.e., a vector which contains the necessary elements for transcriptional and translational control of the inserted coding sequence in a particular host. These elements include regulatory sequences, such as enhancers, constitutive and inducible promoters, and 5' and 3' untranslated regions. Methods which are well known to those skilled in the art may be used to construct such expression vectors. These methods include in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. (See, e.g., Sambrook, supra; and Ausubel, supra).

A variety of expression vector/host cell systems may be utilized to express NSEQ. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast

expression vectors; insect cell systems infected with baculovirus vectors; plant cell systems transformed with viral or bacterial expression vectors; or animal cell systems. For long term production of recombinant proteins in mammalian systems, stable expression in cell lines is preferred. For example, NSEQ can be transformed into cell lines using expression vectors which
5 may contain viral origins of replication and/or endogenous expression elements and a selectable or visible marker gene on the same or on a separate vector. The invention is not to be limited by the vector or host cell employed.

In general, host cells that contain NSEQ and that express PSEQ may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not
10 limited to, DNA-DNA or DNA-RNA hybridizations, PCR amplification, and protein bioassay or immunoassay techniques which include membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein sequences. Immunological methods for detecting and measuring the expression of PSEQ using either specific polyclonal or monoclonal antibodies are known in the art. Examples of such techniques include enzyme-linked
15 immunosorbent assays (ELISAs), radioimmunoassays (RIAs), and fluorescence activated cell sorting (FACS).

Host cells transformed with NSEQ may be cultured under conditions suitable for the expression and recovery of the protein from cell culture. The protein produced by a transgenic cell may be secreted or retained intracellularly depending on the sequence and/or the vector used. As
20 will be understood by those of skill in the art, expression vectors containing NSEQ may be designed to contain signal sequences which direct secretion of the protein through a prokaryotic or eukaryotic cell membrane.

In addition, a host cell strain may be chosen for its ability to modulate expression of the inserted sequences or to process the expressed protein in the desired fashion. Such modifications of
25 the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to specify protein targeting, folding, and/or activity. Different host cells which have specific cellular machinery and characteristic mechanisms for post-translational activities (e.g., CHO, HeLa, MDCK, HEK293, and WI38) are available from the
30 American Type Culture Collection (Manassas VA) and may be chosen to ensure the correct modification and processing of the expressed protein.

In another embodiment of the invention, natural, modified, or recombinant nucleic acid sequences are ligated to a heterologous sequence resulting in translation of a fusion protein containing heterologous protein moieties in any of the aforementioned host systems. Such
35 heterologous protein moieties facilitate purification of fusion proteins using commercially available

affinity matrices. Such moieties include, but are not limited to, glutathione S-transferase, maltose binding protein, thioredoxin, calmodulin binding peptide, 6-His, FLAG, *c-myc*, hemagglutinin, and monoclonal antibody epitopes.

In another embodiment, the nucleic acid sequences are synthesized, in whole or in part, using chemical or enzymatic methods well known in the art (Caruthers *et al.* (1980) Nucleic Acids Symp. Ser. (7) 215-233; Ausubel, *supra*). For example, peptide synthesis can be performed using various solid-phase techniques (Roberge *et al.* (1995) Science 269:202-204), and machines such as the ABI 431A peptide synthesizer (PE Biosystems) can be used to automate synthesis. If desired, the amino acid sequence may be altered during synthesis and/or combined with sequences from other proteins to produce a variant protein.

In another embodiment, the invention entails a substantially purified polypeptide (PSEQ) comprising the amino acid sequence of SEQ ID NO:8 or fragments thereof.

SCREENING, DIAGNOSTICS and THERAPEUTICS

The polynucleotide sequences can be used in selection and evaluation of therapeutic molecules, diagnosis, prognosis, prevention, and treatment for diseases associated with hippocampus, such as Alzheimer's disease, Huntington's disease, schizophrenia, epilepsy, and their complications.

The polynucleotide sequences may be used to screen a library of molecules for specific binding affinity. The assay can be used to screen a library of DNA molecules, RNA molecules, PNAs, peptides, ribozymes, antibodies, agonists, antagonists, immunoglobulins, inhibitors, proteins including transcription factors, enhancers, repressors, and drugs and the like which regulate the activity of the polynucleotide sequence in the biological system. The assay involves providing a library of molecules, combining the polynucleotide sequence or a fragment thereof with the library of molecules under conditions suitable to allow specific binding, and detecting specific binding to identify at least one molecule which specifically binds the polynucleotide sequence.

Similarly the polypeptide or a portion thereof may be used to screen libraries of molecules in any of a variety of screening assays. The portion of the polypeptide employed in such screening may be free in solution, affixed to an abiotic or biotic substrate (e.g. borne on a cell surface), or located intracellularly. Specific binding between the polypeptide and molecule may be measured. The assay can be used to screen a library of DNA molecules, RNA molecules, PNAs, peptides, ribozymes, antibodies, agonists, antagonists, immunoglobulins, inhibitors, peptides, proteins, drugs and the like, which specifically bind the polypeptide. One method for high throughput screening using very small assay volumes and very small amounts of test compound is described in Burbaum *et al.* USPN 5,876,946, incorporated herein by reference, which screens large numbers of molecules for enzyme inhibition or receptor binding.

In one preferred embodiment, the polynucleotide sequences are used for diagnostic purposes to determine the absence, presence, and excess gene expression. The polynucleotides may be at least 18 nucleotides long and consist of complementary RNA and DNA molecules, branched nucleic acids, and/or peptide nucleic acids (PNAs). In one alternative, the polynucleotides are used to detect and quantify gene expression in samples in which expression of NSEQ is correlated with disease. In another alternative, NSEQ can be used to detect genetic polymorphisms associated with a disease. These polymorphisms may be detected in the transcript cDNA.

The specificity of the probe is determined by whether it is made from a unique region, a regulatory region, or from a conserved motif. Both probe specificity and the stringency of diagnostic hybridization or amplification (maximal, high, intermediate, or low) will determine whether the probe identifies only naturally occurring, exactly complementary sequences, allelic variants, or related sequences. Probes designed to detect related sequences should preferably have at least 70% sequence identity to any of the nucleic acid sequences encoding PSEQ.

Methods for producing hybridization probes include the cloning of nucleic acid sequences into vectors for the production of mRNA probes. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes by adding appropriate RNA polymerases and labeled nucleotides. Hybridization probes may incorporate nucleotides labeled by a variety of reporter groups including, but not limited to, radionuclides such as ^{32}P or ^{35}S , enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems, fluorescent labels, and the like. The labeled polynucleotide sequences may be used in Southern or northern analysis, dot blot, or other membrane-based technologies; in PCR technologies; and in microarrays utilizing samples from subjects to detect altered PSEQ expression.

NSEQ can be labeled by standard methods and added to a sample from a subject under conditions suitable for the formation and detection of hybridization complexes. After incubation the sample is washed, and the signal associated with hybrid complex formation is quantitated and compared with a standard value. Standard values are derived from any control sample, typically one that is free of the suspect disease. If the amount of signal in the subject sample is altered in comparison to the standard value, then the presence of altered levels of expression in the sample indicates the presence of the disease. Qualitative and quantitative methods for comparing the hybridization complexes formed in subject samples with previously established standards are well known in the art.

Such assays may also be used to evaluate the efficacy of a particular therapeutic treatment regimen in animal studies, in clinical trials, or to monitor the treatment of an individual subject. Once the presence of disease is established and a treatment protocol is initiated, hybridization or amplification assays can be repeated on a regular basis to determine if the level of expression in the

subject begins to approximate that which is observed in a healthy subject. The results obtained from successive assays may be used to show the efficacy of treatment over a period ranging from several days to many years.

The polynucleotides may be used for the diagnosis of a variety of diseases associated with hippocampus. These include Alzheimer's disease, Huntington's disease, schizophrenia, and epilepsy.

The polynucleotides may also be used as targets in a microarray. The microarray can be used to monitor the expression patterns of large numbers of genes simultaneously and to identify splice variants, mutations, and polymorphisms. Information derived from analyses of the expression patterns may be used to determine gene function, to understand the genetic basis of a disease, to diagnose a disease, and to develop and monitor the activities of therapeutic agents used to treat a disease. Microarrays may also be used to detect genetic diversity, single nucleotide polymorphisms which may characterize a particular population, at the genome level.

In yet another alternative, polynucleotides may be used to generate hybridization probes useful in mapping the naturally occurring genomic sequence. Fluorescent in situ hybridization (FISH) may be correlated with other physical chromosome mapping techniques and genetic map data as described in Heinz-Ulrich et al. (In: Meyers, supra, pp. 965-968).

In another embodiment, antibodies or antibody fragments comprising an antigen binding site that specifically binds PSEQ may be used for the diagnosis of diseases characterized by the over-or-under expression of PSEQ. A variety of protocols for measuring PSEQ, including ELISAs, RIAs, and FACS, are well known in the art and provide a basis for diagnosing altered or abnormal levels of expression. Standard values for PSEQ expression are established by combining samples taken from healthy subjects, preferably human, with antibody to PSEQ under conditions suitable for complex formation. The amount of complex formation may be quantitated by various methods, preferably by photometric means. Quantities of PSEQ expressed in disease samples are compared with standard values. Deviation between standard and subject values establishes the parameters for diagnosing or monitoring disease. Alternatively, one may use competitive drug screening assays in which neutralizing antibodies capable of binding PSEQ specifically compete with a test compound for binding the protein. Antibodies can be used to detect the presence of any peptide which shares one or more antigenic determinants with PSEQ. In one aspect, the anti-PSEQ antibodies of the present invention can be used for treatment or monitoring therapeutic treatment for diseases associated with hippocampus.

In another aspect, the NSEQ, or its complement, may be used therapeutically for the purpose of expressing mRNA and protein, or conversely to block transcription or translation of the mRNA. Expression vectors may be constructed using elements from retroviruses, adenoviruses,

herpes or vaccinia viruses, or bacterial plasmids, and the like. These vectors may be used for delivery of nucleotide sequences to a particular target organ, tissue, or cell population. Methods well known to those skilled in the art can be used to construct vectors to express nucleic acid sequences or their complements. (See, e.g., Maulik *et al.* (1997) Molecular Biotechnology,

5 Therapeutic Applications and Strategies, Wiley-Liss, New York NY.) Alternatively, NSEQ, or its complement, may be used for somatic cell or stem cell gene therapy. Vectors may be introduced *in vivo*, *in vitro*, and *ex vivo*. For *ex vivo* therapy, vectors are introduced into stem cells taken from the subject, and the transgenic cells are clonally propagated for autologous transplant back into that same subject. Delivery of NSEQ by transformation, liposome injections, or polycationic amino
10 polymers may be achieved using methods which are well known in the art. (See, e.g., Goldman *et al.* (1997) *Nature Biotechnol.* 15:462-466.) Additionally, endogenous NSEQ expression may be inactivated using homologous recombination methods which insert an inactive gene sequence into the coding region or other appropriate targeted region of NSEQ. (See, e.g. Thomas *et al.* (1987) *Cell* 51: 503-512.)

15 Vectors containing NSEQ can be transformed into a cell or tissue to express a missing protein or to replace a nonfunctional protein. Similarly a vector constructed to express the complement of NSEQ can be transformed into a cell to downregulate the overexpression of PSEQ. Complementary or antisense sequences may consist of an oligonucleotide derived from the transcription initiation site; nucleotides between about positions -10 and +10 from the ATG are
20 preferred. Similarly, inhibition can be achieved using triple helix base-pairing methodology. Triple helix pairing is useful because it causes inhibition of the ability of the double helix to open sufficiently for the binding of polymerases, transcription factors, or regulatory molecules. Recent therapeutic advances using triplex DNA have been described in the literature. (See, e.g., Gee *et al.* In: Huber and Carr (1994) Molecular and Immunologic Approaches, Futura Publishing, Mt. Kisco
25 NY, pp. 163-177.)

Ribozymes, enzymatic RNA molecules, may also be used to catalyze the cleavage of mRNA and decrease the levels of particular mRNAs, such as those comprising the polynucleotide sequences of the invention. (See, e.g. Rossi (1994) *Current Biology* 4: 469-471.) Ribozymes may cleave mRNA at specific cleavage sites. Alternatively, ribozymes may cleave mRNAs at locations
30 dictated by flanking regions that form complementary base pairs with the target mRNA. The construction and production of ribozymes is well known in the art and is described in Meyers (*supra*).

RNA molecules may be modified to increase intracellular stability and half-life. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3'
35 ends of the molecule, or the use of phosphorothioate or 2' O-methyl rather than phosphodiester

linkages within the backbone of the molecule. Alternatively, nontraditional bases such as inosine, queosine, and wybutosine, as well as acetyl-, methyl-, thio-, and similarly modified forms of adenine, cytidine, guanine, thymine, and uridine which are not as easily recognized by endogenous endonucleases, may be included.

5 Further, an antagonist, or an antibody that binds specifically to PSEQ may be administered to a subject to treat or prevent a disease associated with hippocampus. The antagonist, antibody, or fragment may be used directly to inhibit the activity of the protein or indirectly to deliver a therapeutic agent to cells or tissues which express the PSEQ. An immunoconjugate comprising a PSEQ binding site of the antibody or the antagonist and a therapeutic agent may be administered to
10 a subject in need to treat or prevent disease. The therapeutic agent may be a cytotoxic agent selected from a group including, but not limited to, abrin, ricin, doxorubicin, daunorubicin, taxol, ethidium bromide, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicine, dihydroxy anthracin dione, actinomycin D, diphtheria toxin, Pseudomonas exotoxin A and 40, radioisotopes, and glucocorticoid.

15 Antibodies to PSEQ may be generated using methods that are well known in the art. Such antibodies may include, but are not limited to, polyclonal, monoclonal, chimeric, and single chain antibodies, Fab fragments, and fragments produced by a Fab expression library. Neutralizing antibodies, such as those which inhibit dimer formation, are especially preferred for therapeutic use. Monoclonal antibodies to PSEQ may be prepared using any technique which provides for the
20 production of antibody molecules by continuous cell lines in culture. These include, but are not limited to, the hybridoma, the human B-cell hybridoma, and the EBV-hybridoma techniques. In addition, techniques developed for the production of chimeric antibodies can be used. (See, e.g., Pound (1998) Immunochemical Protocols, Methods Mol. Biol. Vol. 80). Alternatively, techniques described for the production of single chain antibodies may be employed. Antibody fragments
25 which contain specific binding sites for PSEQ may also be generated. Various immunoassays may be used to identify antibodies having the desired specificity. Numerous protocols for competitive binding or immunoradiometric assays using either polyclonal or monoclonal antibodies with established specificities are well known in the art.

Yet further, an agonist of PSEQ may be administered to a subject to treat or prevent a disease
30 associated with decreased expression, longevity or activity of PSEQ.

An additional aspect of the invention relates to the administration of a pharmaceutical or sterile composition, in conjunction with a pharmaceutically acceptable carrier, for any of the therapeutic applications discussed above. Such pharmaceutical compositions may consist of PSEQ or antibodies, mimetics, agonists, antagonists, or inhibitors of the polypeptide. The compositions
35 may be administered alone or in combination with at least one other agent, such as a stabilizing

compound, which may be administered in any sterile, biocompatible pharmaceutical carrier including, but not limited to, saline, buffered saline, dextrose, and water. The compositions may be administered to a subject alone, or in combination with other agents, drugs, or hormones.

The pharmaceutical compositions utilized in this invention may be administered by any number of routes including, but not limited to, oral, intravenous, intramuscular, intra-arterial, intramedullary, intrathecal, intraventricular, transdermal, subcutaneous, intraperitoneal, intranasal, enteral, topical, sublingual, or rectal means.

In addition to the active ingredients, these pharmaceutical compositions may contain suitable pharmaceutically-acceptable carriers comprising excipients and auxiliaries which facilitate processing of the active compounds into preparations which can be used pharmaceutically. Further details on techniques for formulation and administration may be found in the latest edition of Remington's Pharmaceutical Sciences (Maack Publishing, Easton PA).

For any compound, the therapeutically effective dose can be estimated initially either in cell culture assays or in animal models such as mice, rats, rabbits, dogs, or pigs. An animal model may also be used to determine the appropriate concentration range and route of administration. Such information can then be used to determine useful doses and routes for administration in humans.

A therapeutically effective dose refers to that amount of active ingredient which ameliorates the symptoms or condition. Therapeutic efficacy and toxicity may be determined by standard pharmaceutical procedures in cell cultures or with experimental animals, such as by calculating and contrasting the ED_{50} (the dose therapeutically effective in 50% of the population) and LD_{50} (the dose lethal to 50% of the population) statistics. Any of the therapeutic compositions described above may be applied to any subject in need of such therapy, including, but not limited to, mammals such as dogs, cats, cows, horses, rabbits, monkeys, and most preferably, humans.

EXAMPLES

It is to be understood that this invention is not limited to the particular devices, machines, materials and methods described. Although particular embodiments are described, equivalent embodiments may be used to practice the invention. The described embodiments are not intended to limit the scope of the invention which is limited only by the appended claims. The examples below are provided to illustrate the subject invention and are not included for the purpose of limiting the invention. For purposes of example, the preparation of the adult rat hippocampal cDNA library, RAHINOT01, is described.

I cDNA Library Construction

The rat hippocampus cDNA library, RAHINOT01, was constructed from hippocampal tissue removed from a pool of ten, male Sprague Dawley rats (Pharmakon, Waverly PA). The animals were housed in standard laboratory caging and fed PMI-certified Rodent Diet #5002

(Harlan Teklad, Madison WI). The animals appeared to be in good health at the time of tissue harvest. The animals were anesthetized by CO₂ inhalation, and cardiocentesis was performed.

The frozen tissue was homogenized and lysed in TRIZOL reagent (1 g tissue/10 ml; Life Technologies) using a POLYTRON homogenizer (PT-3000; Brinkmann Instruments, Westbury
5 NY). Following homogenization, chloroform was added (1:5 v/v chloroform:homogenate), and the lysate was centrifuged. The aqueous layer was removed, and the RNA was precipitated with isopropanol. The RNA was resuspended in DEPC-treated water.

Messenger RNA (mRNA) was isolated with the OLIGOTEX kit (Qiagen, Valencia CA) and used to construct the cDNA library. The mRNA was handled according to the recommended
10 protocols in the SUPERScript plasmid system (Life Technologies) which contains a NotI primer-adaptor designed to prime the first strand cDNA synthesis at the poly(A) tail of mRNAs. This primer-adaptor contains d(T) residues and restriction endonuclease recognition sites. Three loc-doc primers (Biosource International, Camarillo CA) were synthesized. Each had the same NotI-oligo d(T) primer-adaptor except for a single non-thymine base after the poly(T) segment. This
15 introduced base served to reduce the length of the cloned poly(A) tail. These primers were purified using a SMART SYSTEM HPLC anion exchange column (MiniQ PC 3.2/3, Amersham Pharmacia Biotech (APB), Piscataway NJ) and then combined in an equimolar solution. After cDNA synthesis using SUPERScript reverse transcriptase (Life Technologies) and ligation with EcoRI adaptors, the product was digested with NotI (New England Biolabs, Beverly MA). The cDNAs were
20 fractionated on a SEPHAROSE CL-4B column (APB), and those cDNAs exceeding 400 bp were ligated into the NotI and EcoRI sites of the pINCY plasmid (Incyte Pharmaceuticals). The plasmid was transformed into competent DH5α cells (Life Technologies) or ELECTROMAX DH10B cells (Life Technologies).

II Isolation and Sequencing of cDNA Clones

25 DNA was isolated using the following protocol. Single bacterial colonies were transferred into individual wells of 384-well plates (Genetix Ltd, Christchurch UK) using sterile toothpicks. The wells contained 65 µl of sterile Terrific Broth (Life Technologies) with 25 mg/l carbenicillin and 0.4% glycerol (v/v). The plates were covered and placed in a Thermodyne incubator (Newtown Square PA) at 37°C for 8-10 hours prior to use. Plasmid DNA was released from the cells and
30 amplified using direct link PCR (Rao (1994) Anal. Biochem. 216:1-14). The direct link PCR solution included 30 µl of Nucleix Plus PCR nucleotide mix (APB), 300 µl of Taq DNA polymerase (APB) and 6 µl Pfu DNA polymerase (Stratagene, La Jolla CA). Five microliters of PCR solution were added to each of the 384 wells using the HYDRA 96-well microdispenser system (Robbins Scientific, Sunnyvale CA). The plates were centrifuged at 1000 rpm for 20 seconds and
35 refrigerated until use. A 384 pin tool (V&P Scientific, San Diego CA) was used to transfer

bacterial cells from the incubation plate into the plate containing the PCR solution and 0.1% Tween 20 which lysed the cells and released the plasmid DNA. After lysis, the plates were covered with a cycle sealer, centrifuged up to 500 rpm, and cycled using a 384-well DNA ENGINE TETRAD thermal cycler (MJ Research, Watertown MA) using the program dPCR30 with the following parameters: Step 1) 95°C, 1 minute; Step 2) 94°C, 30 seconds; Step 3) 55°C, 30 seconds; Step 4) 72°C, 2 minutes; Step 5) steps 2, 3, and 4 repeated 29 times; Step 6) 72°C, 10 minutes; and Step 7) storage at 4°C.

The concentration of DNA in each well was determined by dispensing 100 µl PICOGREEN quantitation reagent (Molecular Probes, Eugene OR) (0.25% reagent dissolved in 10 mM TrisHCl, pH 7.5, and 1 mM ethylenediamine tetraacetic acid (EDTA); 1xTE v/v) and 0.5 µl of undiluted PCR product into each well of an opaque fluorimeter plate (Corning Costar, Acton MA) and allowing the DNA to bind to the reagent. The plate was scanned in a Fluoroskan II (Labsystems Oy, Helsinki, Finland) to measure the fluorescence of the sample and to quantify the concentration of DNA.

The cDNAs were prepared using either a MICROLAB 2200 system (Hamilton, Reno NV) or a HYDRA microdispenser (Robbins Scientific, Sunnyvale CA) in combination with the DNA ENGINE thermal cyclers (MJ Research) and sequenced by the method of Sanger and Coulson (1975; J. Mol. Biol. 94:441-448) using an ABI PRISM 377 sequencing system (PE Biosystems). Most of the isolates were sequenced according to standard ABI protocols and kits (PE Biosystems). The solution volumes were used at 0.25x - 1.0x concentrations. In the alternative, cDNAs were sequenced using solutions and dyes from APB.

III Comparative Nucleic Acid Sequence Expression Analysis

Nucleic acid sequences, NSEQ, were first identified in rat tissue using electronic subtraction in the ZOOSEQ database (Incyte Pharmaceuticals) to create a transcript image profile. Target tissue was adult rat hippocampus and background tissue was fetal rat hippocampus. Transcript images for the two rat tissues were compared using the following settings: Stringency ≥ 50 ; product score cutoff ≤ 100 ; and maximum results displayed ALL. Rat clones which were present in the target tissue, but not in the background tissue, were recorded. In addition, rat clones which were present in the background tissue, but not in the target tissue, were recorded. The results included both annotated and unannotated clones. Unannotated clones and clones with annotation descriptions associated with hippocampal tissue were selected. Selected clones were clustered and then assembled using Phrap (P. Green, University of Washington) or GCG Fragment assembly system (Genetics Computer Group (GCG), University of Washington). The resulting rat contigs, SEQ ID NOs:9-15, were queried against LIFESEQ database (Incyte Pharmaceuticals) to identify homologous human nucleic acid sequences using BLAST with the following search parameters:

Expected: 10; expected2: 0.15; Karlin and Atschul sum statistics: and greedy spanning.

Homologous human nucleic acid sequences were clustered and assembled using Phrap or GCG Fragment assembly systems as described above.

VI Homology Searching for Hippocampal Genes and Their Encoded Proteins

5 Polynucleotide sequences, SEQ ID NOs:1-7, and polypeptide sequence. SEQ ID NO:8, were queried against databases derived from sources such as GenBank and SwissProt. These databases, which contain previously identified and annotated sequences, were searched for regions of similarity using BLAST (Altschul, supra). BLAST searched for matches and reported only those that satisfied the probability thresholds of 10^{-25} or less for nucleotide sequences and 10^{-8} or less for
10 polypeptide sequences.

The polypeptide sequence was also analyzed for known motif patterns using MOTIFS, SPSCAN, BLIMPS, and HMM-based protocols. MOTIFS (GCG) searches polypeptide sequences for patterns that match those defined in the Prosite Dictionary of Protein Sites and Patterns (Bairoch supra), and displays the patterns found and their corresponding literature abstracts. SPSCAN
15 (GCG) searches for potential signal peptide sequences using a weighted matrix method (Nielsen et al. (1997) Prot. Eng. 10:1-6). Hits with a score of 5 or greater were considered. BLIMPS uses a weighted matrix analysis algorithm to search for sequence similarity between the polypeptide sequences and those contained in BLOCKS, a database consisting of short amino acid segments, or blocks of 3-6() amino acids in length, compiled from the PROSITE database (Henikoff; supra;
20 Bairoch, supra), and those in PRINTS, a protein fingerprint database based on non-redundant sequences obtained from sources such as SwissProt, GenBank, PIR, and NRL-3D (Attwood et al. (1997) J. Chem. Inf. Comput. Sci. 37:417-424). For the purposes of the present invention, the BLIMPS searches reported matches with a cutoff score of 1000 or greater and a cutoff probability value of 1.0×10^{-3} . HMM-based protocols were based on a probabilistic approach and searched for
25 consensus primary structures of gene families in the protein sequences (Eddy, supra; Sonnhammer, supra). More than 500 known protein families with cutoff scores ranging from 10 to 50 bits were selected for use in this invention.

VII Labeling of Probes and Hybridization Analyses

Polynucleotide sequences are isolated from a biological source and applied to a substrate
30 suitable for standard nucleic acid hybridization protocols by one of the following methods. A mixture of target nucleic acids is fractionated by electrophoresis through an 0.7% agarose gel in 1x TAE running buffer and transferred to a nylon membrane by capillary transfer using 20x saline sodium citrate (SSC). Alternatively, the target nucleic acids are individually ligated to a vector and inserted into bacterial host cells to form a library. Target nucleic acids are arranged on a substrate
35 by one of the following methods. In the first method, bacterial cells containing individual clones are

robotically picked and arranged on a nylon membrane. The membrane is placed on bacterial growth medium, LB agar containing carbenicillin, and incubated at 37°C for 16 hours. Bacterial colonies are denatured, neutralized, and digested with proteinase K. Nylon membranes are exposed to UV irradiation in a STRATALINKER UV-crosslinker (Stratagene, La Jolla CA) to cross-link DNA to
5 the membrane.

In the second method, target nucleic acids are amplified from bacterial vectors by thirty cycles of PCR using primers complementary to vector sequences flanking the insert. Amplified target nucleic acids are purified using SEPHACRYL-400 (APB). Purified target nucleic acids are robotically arrayed onto a glass microscope slide previously coated with 0.05% aminopropyl silane
10 (Sigma-Aldrich, St. Louis MO) and cured at 110°C. The arrayed glass slide (microarray) is exposed to UV irradiation in a STRATALINKER UV-crosslinker (Stratagene).

cDNA probe sequences are made from mRNA templates. Five micrograms of mRNA is mixed with 1 µg random primer (Life Technologies), incubated at 70°C for 10 minutes, and lyophilized. The lyophilized sample is resuspended in 50 µl of 1x first strand buffer (cDNA
15 Synthesis system; Life Technologies) containing a dNTP mix, [α -³²P]dCTP, dithiothreitol, and MMLV reverse transcriptase (Stratagene), and incubated at 42°C for 1-2 hours. After incubation, the probe is diluted with 42 µl dH₂O, heated to 95°C for 3 minutes, and cooled on ice. mRNA in the probe is removed by alkaline degradation. The probe is neutralized, and degraded mRNA and unincorporated nucleotides are removed using a PROBEQUANT G-50 microcolumn (APB).
20 Probes can be labeled with fluorescent nucleotides, Cy3-dCTP or Cy5-dCTP (APB) in place of the radiolabeled nucleotide, [³²P]dCTP.

Hybridization is carried out at 65°C in a hybridization buffer containing 0.5 M sodium phosphate (pH 7.2), 7% SDS, and 1 mM EDTA. After the blot is incubated in hybridization buffer at 65°C for at least 2 hours, the buffer is replaced with 10 ml of fresh buffer containing the probe
25 sequences. After incubation at 65°C for 18 hours, the hybridization buffer is removed, and the blot is washed sequentially under increasingly stringent conditions, up to 40 mM sodium phosphate, 1% SDS, 1 mM EDTA at 65°C. To detect signal produced by a radiolabeled probe hybridized on a membrane, the blot is exposed to a PHOSPHORIMAGER cassette (APB), and the image is analyzed using IMAGEQUANT data analysis software (APB). To detect signals produced by a
30 fluorescent probe hybridized on a microarray, the blot is examined by confocal laser microscopy, and images are collected and analyzed using GEMTOOLS expression analysis software (Incyte Pharmaceuticals).

VIII Production of Specific Antibodies

SEQ ID NO:8, or portions thereof, substantially purified using polyacrylamide gel
35 electrophoresis or other purification techniques, is used to immunize rabbits and to produce

antibodies using standard protocols as described in Pound (supra).

Alternatively, the amino acid sequence is analyzed using LASERGENE software (DNASTAR, Inc.) to determine regions of high immunogenicity, and a corresponding oligopeptide is synthesized and used to raise antibodies by means known to those of skill in the art. Methods for
5 selection of appropriate epitopes, such as those near the C-terminus or in hydrophilic regions are well described in the art. Typically, oligopeptides 15 residues in length are synthesized using an ABI 431A peptide synthesizer (PE Biosystems) using Fmoc-chemistry and coupled to keyhole limpet hemocyanin (KLH; Sigma-Aldrich) by reaction with N-maleimidobenzoyl-N-hydroxysuccinimide ester (Ausubel supra) to increase immunogenicity. Rabbits are immunized with
10 the oligopeptide-KLH complex in complete Freund's adjuvant. Resulting antisera are tested for antipeptide activity by, for example, binding the peptide to plastic, blocking with 1% BSA, reacting with rabbit antisera, washing, and reacting with radio-iodinated goat anti-rabbit IgG.

XII Screening Molecules for Specific Binding with the Nucleic Acid Sequence or Protein

The polynucleotide sequences, or fragments thereof, or the polypeptide, or portions thereof,
15 are labeled with ³²P-dCTP, Cy3-dCTP, Cy5-dCTP (APB), or BIODIPY or FITC (Molecular Probes), respectively. Libraries of candidate molecules; e.g., DNA molecules, RNA molecules, PNAs, peptides, proteins, agonists, antagonists, antibodies, immunoglobulins, inhibitors, and drugs; previously arranged on a suitable substrate are incubated in the presence of labeled polynucleotide sequence or polypeptide. After incubation for a suitable period under appropriate conditions for the
20 polynucleotide sequence or polypeptide, the substrate is washed, and any position on the substrate retaining label, which indicates specific binding or complex formation, is assayed, and the binding molecule is identified. Data obtained using different concentrations of the polynucleotide sequence or polypeptide are used to calculate affinity between the labeled polynucleotide sequence or polypeptide and the bound molecule.

25

TABLE 1

Rat Clone	SEQ ID NO:	Human Clone	Unique Fragment	Identity	Expression Profile
700122146	1	239240	1178-1288	49.7%	Nervous (55%), Endocrine (10%)
700244771	2	350293	719-829	45.2%	Nervous (67%)
700244870	3	244771	1223-1333	63.7%	Nervous (63%), Reproductive (16%)
700025020	4	5308642	717-827	39.2%	Hematopoietic/Immune (22%), Nervous (13%), Digestive System (12%)
700251541	5	2289256	230-340	46.1%	Nervous (50%), Endocrine (38%)
700280514	6	1941247	384-494	76.4%	Nervous (100%)
700024124	7	3864594	636-686	51.0%	Nervous (55%), Reproductive (16%), Hematopoietic/Immune (10%)

What is claimed is:

1. A substantially purified polynucleotide comprising a gene that is expressed in the hippocampus.
2. The polynucleotide of claim 1, comprising a polynucleotide sequence selected from the group consisting of:
 - (a) a polynucleotide sequence selected from the group consisting of SEQ ID NOs:1-7;
 - (b) a polynucleotide encoding a polypeptide sequence consisting of SEQ ID NO:8;
 - (c) a polynucleotide sequence having at least 70% identity to the polynucleotide sequence of (a) or (b);
 - 10 (d) a polynucleotide sequence which is complementary to the polynucleotide sequence of (a), (b) or (c);
 - (e) a polynucleotide sequence comprising at least 18 sequential nucleotides of the polynucleotide sequence of (a), (b), (c), or (d); and
 - (f) a polynucleotide which hybridizes under stringent conditions to the polynucleotide of
 - 15 (a), (b), (c), (d), or (e).
3. A substantially purified polypeptide comprising the gene product of a gene expressed in hippocampus selected from the group consisting of SEQ ID NOs:1-7.
4. The polypeptide of claim 3, comprising
 - (a) a polypeptide sequence of SEQ ID NO:8;
 - 20 (b) a polypeptide sequence having at least 85% identity to the polypeptide sequence of (a);and
 - (c) a polypeptide sequence comprising at least 6 sequential amino acids of the polypeptide sequence of (a) or (b).
5. An expression vector comprising the polynucleotide of claim 2.
- 25 6. A host cell comprising the expression vector of claim 5.
7. The method for producing a protein, the method comprising the steps of:
 - (a) culturing the host cell of claim 6 under conditions suitable for the expression of the protein; and
 - (b) recovering the protein from the host cell culture.
- 30 8. A method of using a polynucleotide sequence or a fragment thereof to screen a library of molecules to identify at least one molecule which specifically binds the nucleic acid, the method comprising:
 - (a) providing a library of molecules.
 - (b) combining the polynucleotide sequence of claim 2 with a library of molecules

under conditions suitable to allow specific binding, and

(c) detecting specific binding, thereby identifying a molecule which specifically binds the polynucleotide sequence.

9. The library of claim 8 wherein the library is selected from the group consisting of: DNA
5 molecules, RNA molecules, PNAs, peptides, ribozymes, antibodies, agonists, antagonists, immunoglobulins, inhibitors, proteins including transcription factors, enhancers, repressors, and drugs.

10. A molecule of claim 9 which modulates the activity of the polynucleotide sequence.

11. A method for using a polypeptide or a portion thereof to screen a library of molecules
10 to identify at least one molecule which specifically binds the polypeptide, the method comprising:
(a) providing a library of molecules,
(b) combining the polypeptide or a portion thereof of claim 4 with the library of molecules under conditions suitable to allow specific binding, and
(c) detecting specific binding, thereby identifying a molecule which specifically
15 binds the polypeptide.

12. The method of claim 11 wherein the library is selected from the group consisting of: DNA molecules, RNA molecules, PNAs, peptides, ribozymes, antibodies, agonists, antagonists, immunoglobulins, inhibitors, peptides, proteins, drugs.

13. A molecule of claim 12 which modulates the activity of the polypeptide.

20 14. A method for diagnosing a disease or condition associated with the altered expression of a gene expressed in hippocampus, the method comprising the steps of:

(a) providing a biological sample;

(b) hybridizing a polynucleotide of claim 2 to the biological sample under conditions effective to form one or more hybridization complexes;

25 (c) detecting the hybridization complexes; and

(d) comparing the levels of the hybridization complexes with the level of hybridization complexes in a non-diseased sample, wherein the altered level of hybridization complexes compared with the level of hybridization complexes of a nondiseased sample correlates with the presence of the disease or condition.

30 15. A method for treating or preventing a disease associated with the altered expression of a gene expressed in hippocampus in a subject in need, the method comprising the step of administering to the subject in need the polynucleotide of claim 2 in an amount effective for treating or preventing a disease selected from the group Alzheimer's disease, Huntington's disease, schizophrenia, epilepsy, and their complications.

16. A method for treating or preventing a disease associated with the altered expression of a gene expressed in hippocampus in a subject in need, the method comprising the step of administering to the subject in need the polypeptide of claim 4 in an amount effective for treating or preventing a disease selected from the group Alzheimer's disease, Huntington's disease, schizophrenia, epilepsy, and their complications.

17. A method for treating or preventing a disease associated with the altered expression of a gene expressed in hippocampus in a subject in need, the method comprising the step of administering to the subject in need the molecule of claim 10 in an amount effective for treating or preventing a disease selected from Alzheimer's disease, Huntington's disease, schizophrenia, and epilepsy.

18. A method for treating or preventing a disease associated with the altered expression of a gene expressed in hippocampus in a subject in need, the method comprising the step of administering to the subject in need the molecule of claim 13 in an amount effective for treating or preventing a disease selected from Alzheimer's disease, Huntington's disease, schizophrenia, and epilepsy.

1/3

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FIGURE 1A

2/3

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FIGURE 1B

3/3

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FIGURE 1C

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 YUE, Henry
 TANG, Tom, Y.
 BAUGHN, Mariah, R.
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International Bureau



(43) International Publication Date
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PCT

(10) International Publication Number
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C07K 14/47

Road, San Leandro, CA 94577 (US). **AZIMZAI, Yalda**
[US/US]; 5518 Boulder Canyon Drive, Castro Valley, CA
94552 (US).

(21) International Application Number: PCT/US00/13046

(22) International Filing Date: 10 May 2000 (10.05.2000)

(74) Agents: **MURRY, Lynn, E.** et al.; Incyte Genomics, Inc.,
3160 Porter Drive, Palo Alto, CA 94304 (US).

(25) Filing Language: English

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ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP,
KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD,
MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD,
SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ,
VN, YU, ZA, ZW.

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Filed on 17 May 1999 (17.05.1999)

(84) Designated States (*regional*): ARIPO patent (GH, GM,
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(AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU,
MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM,
GA, GN, GW, ML, MR, NE, SN, TD, TG).

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Published:

— with international search report

(72) Inventors; and

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(US). **BAUGHN, Mariah, R.** [US/US]; 14244 Santiago

(88) Date of publication of the international search report:
2 August 2001

*For two-letter codes and other abbreviations, refer to the "Guid-
ance Notes on Codes and Abbreviations" appearing at the begin-
ning of each regular issue of the PCT Gazette.*

(54) Title: GENES EXPRESSED IN HIPPOCAMPUS

(57) Abstract: The invention provides novel developmentally-regulated hippocampal genes and polypeptides encoded by those genes. The invention also provides expression vectors, host cells, and antibodies. The invention also provides methods for diagnosing, treating or preventing diseases associated with hippocampus.

WO 00/70036 A3

INTERNATIONAL SEARCH REPORT

International Application No

PC1/US 00/13046

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/12 C07K14/47

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, WPI Data, PAJ, BIOSIS, CHEM ABS Data, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category : Citation of document, with indication, where appropriate, of the relevant passages

Relevant to claim No.

- | | | |
|---|--|---------|
| X | WO 99 06423 A (ENDRESS GREGORY A ;HUMAN
GENOME SCIENCES INC (US); FENG PING (US);
11 February 1999 (1999-02-11)
SEQ ID NO:25 | 2,3,5-8 |
| X | WO 96 12810 A (UNIV EDINBURGH ;LATHE
RICHARD (GB); ROSE KENNETH ANDREW (GB);
STAP) 2 May 1996 (1996-05-02)
abstract | 1 |
| X | PATENT ABSTRACTS OF JAPAN
vol. 2000, no. 02,
29 February 2000 (2000-02-29)
& JP 11 318461 A (SHIOSAKA SADA0;IGAKU
SEIBUTSUGAKU KENKYUSHO:KK),
24 November 1999 (1999-11-24)
abstract | 1 |

☐ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance: the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

20 November 2000

Date of mailing of the international search report

19.02.01

Name and mailing address of the ISA

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Authorized officer

Mata-Vicente, M

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 00/13046

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Claim 1 completely, Claims 2, 3, 5-10, 13-15, 17 partially.

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1 - completely; (2, 3, 5-10, 13-15, 17) - partially

Polynucleotide consisting of SEQ ID NO:1 and derivatives thereof; vector comprising said polynucleotide, host cell transformed with that vector and method for producing a protein involving the culture of said host cell; methods for screening of modulators of the above-mentioned polynucleotide; and methods of diagnosis and treatment involving the same.

2. Claims: (2, 3, 5-10, 13-15, 17) - partially

Idem as in subject 1, but related to SEQ ID NO:2.

3. Claims: (2, 3, 5-10, 13-15, 17) - partially

Idem as in subject 1, but related to SEQ ID NO:3.

4. Claims: (2, 3, 5-10, 13-15, 17) - partially

Idem as in subject 1, but related to SEQ ID NO:4.

5. Claims: (2, 3, 5-10, 13-15, 17) - partially

Idem as in subject 1, but related to SEQ ID NO:5.

6. Claims: (2, 3, 5-10, 13-15, 17) - partially

Idem as in subject 1, but related to SEQ ID NO:6.

7. Claims: (4, 11, 12, 16, 18)- completely; (2, 3, 5-10, 13-15, 17) - partially

Polynucleotide consisting of SEQ ID NO:7 and polypeptide of SEQ ID NO:8, and derivatives thereof; vector comprising said polynucleotide, host cell transformed with that vector and method for producing a protein involving the culture of said host cell; methods for screening of modulators of the polynucleotide and the polypeptide mentioned above; and methods of diagnosis and treatment involving the same.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/13046

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9906423	A	11-02-1999	AU 8763498 A EP 1003763 A	22-02-1999 31-05-2000
WO 9612810	A	02-05-1996	AU 711903 B AU 3670395 A CA 2203105 A EP 0795017 A JP 10512739 T NZ 294019 A US 5976850 A	21-10-1999 15-05-1996 02-05-1996 17-09-1997 08-12-1998 28-05-1999 02-11-1999
JP 11318461	A	24-11-1999	NONE	

